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☐ 1: Jones AL, Hulett MD, Parish CR.

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Histidine-rich glycoprotein binds to cell-surface heparan sulfate via its N-terminal domain following Zn²⁺ chelation.

J Biol Chem. 2004 Jul 16;279(29):30114-22. Epub 2004 May 11.

PMID: 15138272 [PubMed - in process]

☐ 2: Kim BT, Kim WS, Kim YS, Linhardt RJ, Kim DH.

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Purification and characterization of a novel heparinase from Bacteroides stercoris HJ-15.

J Biochem (Tokyo). 2000 Aug;128(2):323-8.

PMID: 10920269 [PubMed - indexed for MEDLINE]

☐ 3: Pejasek K, Shriver Z, Hu Y, Sasisekharan R.

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Histidine 295 and histidine 510 are crucial for the enzymatic degradation of heparan sulfate by heparinase III.

Biochemistry. 2000 Apr 11;39(14):4012-9.

PMID: 10747789 [PubMed - indexed for MEDLINE]

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DT Utility; Patent Application - First Publication
FS CHEMICAL APPLICATION

CLMN 60

GI 16 Figure(s).

FIG. 1 is a graph depicting the effect of DEPC inactivation of heparinase III on rate constant.

FIG. 2 is a graph depicting the pH dependence of the second order rate constant of inactivation upon incubation of heparinase III with varying concentrations of DEPC.

FIG. 3 is a graph depicting the quantification of DEPC-modified **histidine** residues in **heparinase III** over a period of time.

FIG. 4 is a graph depicting the substrate protection of heparinase III. inactivation by DEPC III.

FIG. 5 is a reverse phase HPLC profile of a lys-C digest of heparinase III which was not exposed to DEPC (top panel) and a peptide profile of heparinase III labeled with DEPC (bottom panel).

FIG. 6 is a series of graphs depicting SAX analysis of exhaustive heparinase III digests of heparan sulfate. Heparan sulfate was digested with either heparinase III from F. heparinum (panel A), recombinant heparinase III (panel B), H295A mutant enzyme (panel C), H510A mutant enzyme (panel D), or the H105A mutant enzyme (panel E).

FIG. 7 depicts a circular dichroism analysis of recombinant heparinase III and the H295A mutant enzyme, and the H510A mutant enzyme.

FIG. 8 is a graph depicting tumor volume in mice, as well as mice treated with heparinase I.

FIG. 9 is a bar graph depicting number of lung nodules that developed 13 days after tail vein injection of B16 BL6 cells. The cells were either

treated with PBS, heparinase I, or heparinase III.
 FIG. 10, panel A, depicts the tumor volume of mice that were treated with GAG fragments generated from treatment of B16 BL6 cells with either heparinase I, heparinase III, or PBS or fragments generated from heparinase I treatment of LLC cells. Tumor volume was measured over time between 7 and 15 days postinjection of the tumor cells.
 FIG. 10, panel B is a bar graph which quantitates the number of lung nodules of the mice described in panel A.
 FIG. 11 is a bar graph depicting the effect on B16 cellular migration and invasion of transfection with antisense 2OST in pcDNA3.1.
 FIG. 12 shows bar graphs depicting the ability of the transfected cells of FIG. 12 to develop into primary tumors as assessed by mean tumor volume (12a) and tumor weight (12b).
 FIG. 13 depicts the results of compositional analysis of HLGAG saccharide fragments released from B16BL6 cells.
 FIG. 14 is a bar graph depicting FGF2 signaling modulated by HLGAG fragments
 FIG. 15 is a table (15a) and a schematic depicting the modulation of FGF2 activity in vivo by B16BL6 fragments (15b).

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 FIG. 1 is a graph depicting the effect of DEPC inactivation of heparinase III on rate constant.
 FIG. 2 is a graph depicting the pH dependence of the second order rate constant of inactivation upon incubation of heparinase III with varying concentrations of DEPC.
 FIG. 3 is a graph depicting the quantification of DEPC-modified **histidine** residues in **heparinase III** over a period of time.
 FIG. 4 is a graph depicting the substrate protection of heparinase III inactivation by DEPC III.
 FIG. 5 is a reverse phase HPLC profile of a lys-C digest of heparinase III which was not exposed to DEPC (top panel) and a peptide profile of heparinase III labeled with DEPC (bottom panel).
 FIG. 6 is a series of graphs depicting SAX analysis of exhaustive heparinase III digests of heparan sulfate. Heparan sulfate was digested with either heparinase III from F. heparinum (panel A), recombinant heparinase III (panel B), H295A mutant enzyme (panel C), H510A mutant enzyme (panel D), or the H105A mutant enzyme (panel E).
 FIG. 7 depicts a circular dichroism analysis of recombinant heparinase III and the H295A mutant enzyme, and the H510A mutant enzyme.
 FIG. 8 is a graph depicting tumor volume in mice, as well as mice treated with heparinase I.
 FIG. 9 is a bar graph depicting number of lung nodules that developed 13 days after tail vein injection of B16 BL6 cells. The cells were either treated with PBS, heparinase I, or heparinase III.

FIG. 10, panel A, depicts the tumor volume of mice that were treated with GAG fragments generated from treatment of B16 BL6 cells with either heparinase I, heparinase III, or PBS or fragments generated from heparinase I treatment of LLC cells. Tumor volume was measured over time between 7 and 15 days postinjection of the tumor cells.

FIG. 10, panel B is a bar graph which quantitates the number of lung nodules of the mice described in panel A.

FIG. 11 is a bar graph depicting the effect on B16 cellular migration and invasion of transfection with antisense 20ST in pcDNA3.1.

FIG. 12 shows bar graphs depicting the ability of the transfected cells of FIG. 12 to develop into primary tumors as assessed by mean tumor volume (12a) and tumor weight (12b).

FIG. 13 depicts the results of compositional analysis of HLGAG saccharide fragments released from B16BL6 cells.

FIG. 14 is a bar graph depicting FGF2 signaling modulated by HLGAG fragments

FIG. 15 is a table (15a) and a schematic depicting the modulation of FGF2 activity in vivo by B16BL6 fragments (15b).

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AN 2002:39656 DISSABS Order Number: AAI0803378

TI Sequencing complex polysaccharides

AU Shriver, Zachary [Ph.D.]; Sasisekharan, Ram [adviser]

CS Massachusetts Institute of Technology (0753)

SO Dissertation Abstracts International, (2001) Vol. 63, No. 1B, p. 380. Order No.: AAI0803378.

DT Dissertation

FS DAI

LA English

L2 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 3

AN 2000:313840 BIOSIS

DN PREV200000313840

TI Histidine 295 and histidine 510 are crucial for the enzymatic degradation of heparan sulfate by heparinase III.

AU Pojasek, Kevin; Shriver, Zachary; Hu, Yini; Sasisekharan, Ram [Reprint author]

CS 16-561, MIT, Cambridge, MA, 02139, USA

SO Biochemistry, (April 11, 2000) Vol. 39, No. 14, pp. 4012-4019. print. CODEN: BICHAW. ISSN: 0006-2960.

DT Article

LA English

ED Entered STN: 26 Jul 2000

Last Updated on STN: 7 Jan 2002

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L2 ANSWER 6 OF 6 GENBANK® COPYRIGHT 2004 on STN

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GenBank ACC. NO. (GBN): AL939105 AL109974 AL117385 AL117387 AL117669 AL121596 AL121600 AL121719 AL121849 AL121855 AL132662 AL132707 AL645882

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 DIVISION CODE (CI): Bacteria
 DATE (DATE): 11 Feb 2003
 DEFINITION (DEF): Streptomyces coelicolor A3(2) complete genome; segment 2/29.
 SOURCE: Streptomyces coelicolor A3(2)
 ORGANISM (ORGN): Streptomyces coelicolor A3(2)
 Bacteria; Actinobacteria; Actinobacteridae;
 Actinomycetales; Streptomycineae; Streptomycetaceae;
 Streptomyces
 NUCLEIC ACID COUNT (NA): 39089 a 105537 c 106715 g 39659 t
 COMMENT:

On or before Oct 29, 2002 this sequence version replaced
 gi:20520891, gi:20520894, gi:20520895, gi:20520772, gi:20520896,
 gi:20520897, gi:20520883, gi:20520899, gi:20520902.

REFERENCE: 1
 AUTHOR (AU): Bentley, S.D.; Chater, K.F.; Cerdeno-Tarraga, A.M.;
 Challis, G.L.; Thomson, N.R.; James, K.D.; Harris, D.E.;
 Quail, M.A.; Kieser, H.; Harper, D.; Bateman, A.; Brown, S.;
 Chandra, G.; Chen, C.W.; Collins, M.; Cronin, A.;
 Fraser, A.; Goble, A.; Hidalgo, J.; Hornsby, T.;
 Howarth, S.; Huang, C.H.; Kieser, T.; Larke, L.; Murphy, L.;
 Oliver, K.; O'Neil, S.; Rabinowitsch, E.;
 Rajandream, M.A.; Rutherford, K.; Rutter, S.; Seeger, K.;
 Saunders, D.; Sharp, S.; Squares, R.; Squares, S.;
 Taylor, K.; Warren, T.; Wietzorrek, A.; Woodward, J.;
 Barrell, B.G.; Parkhill, J.; Hopwood, D.A.
 TITLE (TI): Complete genome sequence of the model actinomycete
 Streptomyces coelicolor A3(2)
 JOURNAL (SO): Nature, 417 (6885), 141-147 (2002)
 OTHER SOURCE (OS): CA 136:396750
 REFERENCE: 2 (bases 1 to 291000)
 AUTHOR (AU): Bentley, S.D.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (09-MAY-2002) Submitted on behalf of the
 Streptomyces sequencing team, Sanger Institute,
 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10
 1SA E-mail: sdb@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..291000	/organism="Streptomyces coelicolor A3(2)" /strain="A3(2)" /db-xref="taxon:100226"
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CDS	213..3092	/gene="SCO0305" /note="SC5G9.14, hypothetical protein, len: 959 aa; unknown function, similar to TR:O54182 (EMBL:AL021411) Streptomyces coelicolor hypothetical protein (913 aa), fasta scores; opt: 698 z-score: 776.6 E(): 0, 27.0% identity in 972 aa overlap. The C-terminus shows very weak similarity to eukaryotic beta-transducins e.g. SW:GBB4-MOUSE (EMBL:S86124), gnb4,

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 in 291 aa overlap). Contains
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 frameplot and codon usage plots
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CDS	4084..4971	/gene="SCO0307"
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gene	5026..6429	/gene="SCO0308"
		/note="synonym: SC5G9.17"
CDS	5026..6429	/gene="SCO0308"
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		ELLVESFHASLRDVSLLADALANT SRIVERVNAVLRVGLTAAQQYAEDRDRVLA AVIAAGSLLALPPALLLAYFGVNS SDVDPSRSILDFQHGYGAYAIWSPFLLLILVGL LARRRISLRLPAPDAATSERRTRR FRRSLRSWLGRSRRPGR"
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gene	complement(6537..7625)	/gene="SCO0309" /note="synonym: SC5G9.18c"
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CDS	complement (7816..8466)	<p> / gene="SC00310" / note="synonym: SC5G9.19c" / gene="SC00310" / note="SC5G9.19c, possible tetR-family transcriptional regulator, len: 141 aa; shows similarity to the N-terminal half of TR:O24741 (EMBL:AB001683), FarA, Streptomyces sp. strain FRI-5 receptor for an extracellular regulatory factor (IM-2) (221 aa), fasta scores; opt: 154 z-score: 193.4 E(): 0.0021, 36.7% identity in 79 aa overlap and to putative transcriptional regulators: Contains Pfam match to entry </p>

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misc-feature	complement (8278..8418)	/gene="SCO0310"
		/note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 31.50, E-value 5.4e-07"
gene	8575..10131	/gene="SCO0311"
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CDS	8575..10131	/gene="SCO0311"
		/note="SC5G9.20, probable ligase, len: 518 aa; similar to domains within polyketide synthases e.g. to the N-terminus of TR:Q54297 (EMBL:X86780), RapA, Streptomyces hygroscopicus polyketide synthase (8563 aa), fasta scores; opt: 815 z-score: 894.4 E(): 0, 34.0% identity in 509 aa overlap and to SW:DHBE-BACSU (EMBL:U26444), DhbE, EntE, Bacillus subtilis 2,3-dihydroxybenzoate-AMP ligase (539 aa) (31.3% identity in 520 aa overlap). Also similar to others from S. coelicolor e.g. TR:Q9Z5A6 (EMBL:AL035478) S. coelicolor probable long-chain-fatty-acid-CoA ligase (541 aa) (35.9% identity in 537 aa overlap). Contains Pfam match to entry PF00501 AMP-binding, AMP-binding enzyme and PS00455 Putative AMP-binding domain signature"
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		GVLFLSTEDHRRAVEGDDEELLS CGRPLAAEVRIVDDGGEPVADGEIGEIAVRGPD VVPGYHNEPELTARSFRDGFMTG DLARRRRDGYVFIVDRKKDMIISGGFNIYAVEVE SVLHQHPDVFEAAVVGVPDEQWGE AVKAVVVPRAVTLDATELIAFCAEHLARMKKPR SVDVVAALPHNPNGKIDRRRAIRD YWSGAERRVH"
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misc-feature	9055..9090	/gene="SCO0311" /note="PS00455 Putative AMP-binding domain signature"
gene	10147..11316	/gene="SCO0312" /note="synonym: SC5G9.21"
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		/note="SC5G9.23, putative secreted protein, len: 648 aa; unknown function, similar to TR:Q52556 (EMBL:M86744), SdsA, Pseudomonas sp. alkyl sulfatase which degrades sulfate esters of long-chain primary alcohols (SDS) (528 aa), fasta scores; opt: 739 z-score: 806.7 E(): 0, 29.7% identity in 528 aa overlap, but having an N-terminal extension of approx. 140 aa. Similar to TR:Q48790

(EMBL:X92423), SepA, *Listeria monocytogenes* gene implicated in cell separation (391 aa) (42.6% identity in 364 aa overlap). Also similar to hypothetical proteins e.g. TR:069728 (EMBL:AL022121) *Mycobacterium tuberculosis* hypothetical protein (626 aa) (52.9% identity in 624 aa overlap). Contains Pfam match to entry PF00753 lactamase-B, Metallo-beta-lactamase superfamily. Contains possible N-terminal region signal sequence peptide"

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/note="SC5G9.24c, probable decarboxylase, len: 452 aa; similar to many e.g. SW:DCDA-BACSU (EMBL:L09228), LysA, *Bacillus subtilis* diaminopimelate decarboxylase (441 aa), fasta scores; opt: 484 z-score: 542.1 E(): 7.9e-23, 31.6% identity in

389 aa overlap. Similar to
 TR:Q9ZBH5 (EMBL:AL035206), DcdA,
 Streptomyces coelicolor
 diaminopimelate decarboxylase (440
 aa), fasta scores; opt: 400
 z-score: 384.5 E(): 3.6e-16, 30.2%
 identity in 427 aa overlap.
 Contains 2 Pfam matches to entry
 PF00278 Orn-DAP-Arg-deC,
 Pyridoxal-dependent decarboxylase,
 PS00879 Orn/DAP/Arg decarboxylases
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)
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 decarboxylases family 2 signature
 2"

misc-feature complement(15816..15872
)
 /note="PS00878 Orn/DAP/Arg
 decarboxylases family 2
 pyridoxal-P attachment site"

gene complement(16254..17921
)
 /note="synonym: SC5G9.25c"

CDS complement(16254..17921
)
 /note="SC5G9.25c, hypothetical

protein, len: 555 aa; similar to
hypothetical proteins e.g.
TR:O50442 (EMBL:AL010186)
Mycobacterium tuberculosis
hypothetical protein (538 aa),
fasta scores; opt: 485 z-score:
521.2 E(): 1.2e-21, 32.6% identity
in 568 aa overlap and to TR:Q9Z561
(EMBL:AL035569) S.coelicolor
putative transcriptional regulator
(415 aa) (28.4% identity in 444 aa
overlap). Contains probable
helix-turn-helix motif at aa
505-526 (Score 1081, +2.87 SD)"
/codon-start=1
/transl-table=11
/product="putative DNA-binding
protein"
/protein-id="CAB55673.1"
/db-xref="GI:5881873"
/translation="MAAREPDRRDGRPSLEQILR
LIAPGMLDVVVAPRGTVGPVADAV
LHDPGEERDDGTWAASGLILLAVGVDAAPAEID
VLRGAERAGAAAVLRRGARGPRA
ALLEAAASGRRTALLTRRPGQGWTEVLGQLRTALA
HSAPTGGTGVGELRLGDLPELANT
VAALVGGAITIEDPQSRVLAYS SRMDHEPDPMRRL
TILGQEVPRWRVDELRESGFFQAL
WNTDGVVRLPADDYAERLAVAVRHGSEILGSLW
AADGRPLAEDAAAALHTAARAAV
PHLAHHQTWGRAAAARARESAVHALLDGSGPAARV
AHDAGVAPDRPYTVLVAEAYDSRD
LTAVPAPATGGAAGQRTLDVLALQAEAYRPGCVT
ARSGRRLYVLI PAEDGETDPARAL
TATARSVPRGVVFAGVGPVAADLSGLPASREAAE
LVVRVLREERAARRPAADVVSAAV
FGEVVPEVSALRVLDLIAPLWQSLSGPVHAMVEH
DRAHGSEYGASVGAYLDAFGDTGT
AAQRLNVHPNLTLYRLRRARELFGVDLADPTLRL
LADVGLRLARRTE"

gene complement(17975..19237 /gene="SCO0317"
)

CDS complement(17975..19237 /gene="SCO0317"
)
/note="synonym: SC5G9.26c"

/note="SC5G9.26c, probable
transmembrane transport protein,
len: 420 aa; shows weak similarity
to many efflux pumps e.g.
SW:CMLR-STRLI (EMBL:X59968), cmlR,
Streptomyces lividans
chloramphenicol resistance protein
(392 aa), fasta scores; opt: 276
z-score: 292.9 E(): 6e-09, 27.3%
identity in 407 aa overlap.
Contains hydrophobic, possible
membrane-spanning regions"
/codon-start=1
/transl-table=11
/product="putative transmembrane
transport protein"
/protein-id="CAB55674.1"
/db-xref="GI:5881874"

```

/translation="MSERATESVLRSPGIPHLLT
VGAFCFAGLALLLPVSPAWAVAGG
ADEFAGGLVTAVLMAATVLAQLCVRTALRTIGWP
RTLALGALLLGLPALVQSLSDHLV
PILVTTALRGAGFGI VTCGATAAAALAPRGRQG
AAIGLYGLAVALPQVILTPAAPWL
MGTFALPAIVACGVLPVLALPWTRALGRAVEART
DGPPTQDGRTGHPAPAATVLRRL
LPLTVLLLVTAAAGAVLTFAPQFTSTPALAATGL
LALTATAALARWGC GELADRIALR
PITALLASTACAGLALIALAVGPDGETVLP LLAG
LLLLGTAYGGLQSLTLVQAFDLG
AEDRHMTSVAWNIGYDAGTGLGSLALGLAAQAAT
FSAGFAVMSAVMAAVVLAVLLTPG
RPAGRTAGDRPRTSRTRRRSPARPKLP"
gene      complement(19329..20345 /gene="SCO0318"
)
CDS      complement(19329..20345 /gene="SCO0318"
)
/translation="MGESVLLTSTPPEHKESVIV
SSAPQSRPVDVHRLPSAEGRNFLV
TGGNAGIGYFTAELAATGALVVIGSRNPAKADA
ALASIRSRVPGARVRHLHLDLADL
STLKS AVDGLALDLGRLDAVVHNAGGALDDPPRR
ETEDGHELMFGTNHLGHYALTRWL
APLLSAAPAGRVVTVGSFAARSERLDLDDLQSTR
DYPKRTYGRSKLAQMCFGFELDR
RLRAAGSTVLSAVAHPPGALDSLTPPRPPVGAPT
PGERLRGLPAALMVQGGKAGAWPV
VRAVLDSVQGGQLWGPVFLRGQPRREPVPAP
MADPAVAARLWAASAELTGTTDPH LGFR"
misc-feature complement(19626..20228 /gene="SCO0318"
)

```

/note="synonym: SC5G9.27c"

/note="SC5G9.27c, possible
oxidoreductase, len: 388 aa; shows
weak similarity to many eukaryotic
and bacterial oxidoreductases e.g.
TR:Q39617 (EMBL:U36752), LpcR-1,
Chlamydomonas reinhardtii
NADPH:protochlorophyllide
oxidoreductase (397 aa), fasta
scores; opt: 278 z-score: 296.3
E(): 3.8e-09, 27.4% identity in
343 aa overlap. Similar to
TR:O53726 (EMBL:AL021932)
Mycobacterium tuberculosis
putative oxidoreductase (311 aa)
(41.1% identity in 309 aa
overlap). Similar to others from
S. coelicolor e.g. SCJ9A.19c
(cosmid SCJ9A), possible
oxidoreductase (311 aa) (39.6%
identity in 303 aa overlap).
Contains Pfam match to entry
PF00106 adh-short, short chain
dehydrogenase"

/codon-start=1
/transl-table=11
/product="putative oxidoreductase"
/protein-id="CAB55675.1"
/db-xref="GI:5881875"
/translation="MGESVLLTSTPPEHKESVIV
SSAPQSRPVDVHRLPSAEGRNFLV
TGGNAGIGYFTAELAATGALVVIGSRNPAKADA
ALASIRSRVPGARVRHLHLDLADL
STLKS AVDGLALDLGRLDAVVHNAGGALDDPPRR
ETEDGHELMFGTNHLGHYALTRWL
APLLSAAPAGRVVTVGSFAARSERLDLDDLQSTR
DYPKRTYGRSKLAQMCFGFELDR
RLRAAGSTVLSAVAHPPGALDSLTPPRPPVGAPT
PGERLRGLPAALMVQGGKAGAWPV
VRAVLDSVQGGQLWGPVFLRGQPRREPVPAP
MADPAVAARLWAASAELTGTTDPH LGFR"

/note="Pfam match to entry PF00106"

		adh-short, short chain dehydrogenase, score 70.30, E-value 4e-17"
gene	complement(20499..21008)	/gene="SCO0319"
CDS	complement(20499..21008)	/note="synonym: SC5G9.28c" /gene="SCO0319"
		/note="SC5G9.28c, unknown, len: 169 aa; probable CDS suggested by GC frameplot, positional base preference and amino acid composition" /codon-start=1 /transl-table=11 /product="hypothetical protein SC5G9.28c" /protein-id="CAB55676.1" /db-xref="GI:5881876" /translation="MEAESGHAVVHQCGGRHRGQ PSGNRHDLRLTRDDLFVSGPGSH DHTPADPARVHVSVTDQCQHLARPAATRHVRQRARE EVLTPAAAQQRVQEDDVGRDHTDD DLAGAGHGIGQVDQAQHVRSTERGHVDRMHEQHP SLEATSRPASNLKSGRGQGSSVVR GGVGPVGKG"
gene	21110..21583	/gene="SCO0320"
CDS	21110..21583	/note="synonym: SC5G9.29" /gene="SCO0320"
		/note="SC5G9.29, hypothetical protein, len: 157 aa; similar to the C-terminal half of SW:QOR-PSEAE (EMBL:X85015), qor, Pseudomonas aeruginosa quinone oxidoreductase (325 aa), fasta scores; opt: 223 z-score: 254.4 E(): 8.3e-07, 34.8% identity in 161 aa overlap and the corresponding region of many similar hypothetical proteins. Also similar to regions of polyketide synthase-type proteins e.g. SW:MCAS-MYCBO (EMBL:M95808), mas, Mycobacterium bovis mycocerosic acid synthase (2110 aa) (35.8% identity in 159 aa overlap). Contains PS00017 ATP/GTP-binding site motif A (P-loop)" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAB55677.1" /db-xref="GI:5881877" /translation="MVAAASSDAKLALARDLGAE VVVDYTRADWVERVREATGGGAAL VYDGAGGALGATSVDALADGGRFVTYGTADGFAA PDRESAARRGIRLLMPLMDGPPDQ ETARELLGLALESAAEGRLRPAIGATYPLARAAD AHRALAARTTVGKSLLLMGGE"
misc-feature	21536..21559	/gene="SCO0320" /note="PS00017 ATP/GTP-binding site motif A (P-loop)"

gene	21699..23255	/gene="SCO0321"
		/note="synonym: SC5G9.30"
CDS	21699..23255	/gene="SCO0321"
		/note="SC5G9.30, probable carboxylesterase, len: 518 aa; similar to many eukaryotic and bacterial e.g. SW:PNBA-BACSU (EMBL:U06089), PrnBA, Bacillus subtilis 4-nitrobenzyl esterase (489 aa), fasta scores; opt: 718 z-score: 774.9 E(): 0, 36.3% identity in 479 aa overlap. Similar to TR:Q9Z545 (EMBL:AL035212) Streptomyces coelicolor probable carboxylesterase (502 aa) (41.3% identity in 521 aa overlap). Contains 2 Pfam matches to entry PF00135 COesterase, Carboxylesterases and PS00122 Carboxylesterases type-B serine active site"
		/codon-start=1
		/transl-table=11
		/product="putative carboxylesterase"
		/protein-id="CAB55678.1"
		/db-xref="GI:5881878"
		/translation="MQREAVPVVFKTRHGSRVG FRASGDVVAVLGVPYAAAPFGVHR FREPAAPAWTGVDRSFGPVPQASARLPGAPV WSPGDEDILTWNLTWPAPDGGPLP VLVWIHGGAYTFGSSAQPDFDGTVLARAGLVVVT LNYRIGFEGFGHVPPDGPIAHFDPN RGLLDQVAALRWVRENIAAFGGEPGNVTVAGQSS GAASVACLMVMDRARGLFHRAIAH SPASPCYPRDIAAATTREVAAAAGCPATSAGLRS TTPQALVAAADQVADGYRRDPASG SRHYDPSLYAPVLDDDLPTDPLTGMAAGAARDV DLLVCHTTEEYWLLDAVGSSAKVT TDAQLARFAEDFGLPDGLVAGYRAALPRAPVLDV YLAVFGDLLFGEYANRLAEVHARA GGRAFLSRFDRRRADPGAVVRAWHCADVPFAFGN LDDERLAFLIGGAPTAADQGLARR MVRWADFAATGSPGWPPVRDSSTEATEATEATE AKVWTADPHAARTGDRAAAVRALW AEADFPVLRP"
misc-feature	21735..22658	/gene="SCO0321"
		/note="Pfam match to entry PF00135 COesterase, Carboxylesterases, score 250.70, E-value 2.9e-72"
misc-feature	22236..22283	/gene="SCO0321"
		/note="PS00122 Carboxylesterases type-B serine active site"
misc-feature	22944..23186	/gene="SCO0321"
		/note="Pfam match to entry PF00135 COesterase, Carboxylesterases, score 12.90, E-value 0.0041"
gene	complement(23244..24938)	/gene="SCO0322"
		/note="synonyms: SC5G9.31c, SCF12.01c"
CDS	complement(23244..24938	/gene="SCO0322"

)

/note="SCF12.01c, possible ABC
transport ATP-binding subunit,
len: >230aa; similar to many eg.
SW:TLRC-STRFR tylosin resistance
ATP-binding protein from
Streptomyces fradiae (548 aa)
fasta scores; opt: 1017, z-score:
1131.8, E(): 0, (69.0% identity in
232 aa overlap). Contains Prosite
match to PS00211 ABC transporters
family signature and Prosite match
to PS00017 ATP/GTP-binding site
motif A (P-loop). SC5G9.31c,
probable ABC-transporter
ATP-binding protein, partial CDS,
len: >371 aa; similar ATP-binding
components from antibiotic
resistance export systems e.g.
SW:TLRC-STRFR (EMBL:M57437), tlrC,
Streptomyces fradiae tylosin
resistance ATP-binding protein
(548 aa), fasta scores; opt: 1517
z-score: 1597.3 E(): 0, 67.4%
identity in 356 aa overlap. Also
similar to many other putative
ABC-transporter ATP-binding
proteins. Contains Pfam match to
entry PF00005 ABC-tran, ABC
transporter, PS00211 ABC
transporters family signature and
PS00017 ATP/GTP-binding site motif
A (P-loop)"
/codon-start=1
/transl-table=11
/product="putative ABC transport
ATP-binding subunit"
/protein-id="CAD55436.1"
/db-xref="GI:24418992"
/translation="MRTSQLTLSHVTKRYAGRVT
LDQVSLTLKPGEKAGLIGDNGAGK
STLLRIVAGQERPDSGEATVTAAGGIGCLPQSV
LPPTATVQDAVDLSLADLRALAE
LRRAEQALGAGEDPEALAAITVLVERYEARDGHD
ADRRVDIALHHLGLPALRRERRLG
TLSGGERSRLALAGVLAGRPEVLLLDEPTNDLDD
QAVEWLETQLRAHRGTVLAVTHDR
VFLERLTSTILEAEGGRVTRYGDGYNGYRTAKAA
ERRRRLQEHEEWRSELARNERLAT
GHAARLGAI PRKASLANFGHGGFRARGRAHGAMS
RIRNARERVERLTENPVAPPPDAL
AFTVRMATAAEEASATGAASATLPAVQLSDVRVG
DRLHLGSLGLGRRGRLLVITGPNGA
GKT'TLLKVLAGELRPDEGSVRVPGRVGHRLRQEET
PWPPELTVAEAFGLGRVGADEHA
DTLLALGLFRPAELRLRMGELSYGQRRRVELARL
VSEPVDLLLLDEPTNHLSPALVEE
LEEALTGFSGAIVLVTHDRALRGRFRGRRLTLPA
APGARTGQPVAVAHRPRPGSGA"
/gene="SCO0322"

misc-feature

complement (23310..23798

)

/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score

144.30, E-value 2.1e-39"